

What is claimed is:

1. A composition comprising nucleic acid molecules containing a human sequence encoding insulin-like growth factor (hIGF) substantially free of nucleic acid molecules not containing said hIGF sequence, wherein said hIGF sequence is selected from the group consisting of:

(a) 5'-GGA CCG GAG ACG CUC UGC GGG GCU GAG CUG GUG GAU GCU CUU CAG UUC GUG UGU GGA GAC AGG GGC UUU UAU UUC AAC AAG CCC ACA GGG UAU GGC UCC AGC AGU CGG AGG GCG CCU CAG ACA GGU AUC GUG GAU GAG UGC UGC UUC CGG AGC UGU GAU CUA AGG AGG CUG GAG AUG UAU UGC GCA CCC CUC AAG CCU GCC AAG UCA GCU-3', wherein U can also be T;

(b) 5'-GCU UAC CGC CCC AGU GAG ACC CUG UGC GGC GGG GAG CUG GUG GAC ACC CUC CAG UUC GUC UGU GGG GAC CGC GGC UUC UAC UUC AGC AGG CCC GCA AGC CGU GUG AGC CGU CGC AGC CGU GGC AUC GUU GAG GAG UGC UGU UUC CGC AGC UGU GAC CUG GCC CUC CUG GAG ACG UAC UGU GCU ACC CCC GCC AAG UCC GAG-3', wherein U can also be T;

(c) nucleic acid sequences complementary to (a) or (b); and

(d) fragments of (a), (b) or (c) that are at least 18 bases in length and which will selectively hybridize to human genomic DNA encoding hIGF.

2. A composition according to claim 1 wherein said hIGF is hIGF-I and said hIGF sequence is sequence (a).

3. A composition according to claim 1 wherein said hIGF is hIGF-II and said hIGF sequence is sequence (b).

4. A composition according to claim 2 wherein said nucleic acid molecules comprise the following sequence, wherein U can also be T:

5'-CUG GCG CUG UGC CUG CUC ACC UUC ACC AGC UCU GCC ACG GCU GGA CCG GAG ACG CUC UGC GGG GCU GAG CUG GUG GAU GCU CUU CAG UUC GUG UGU GGA GAC AGG GGC UUU UAU UUC AAC AAG CCC ACA GGG UAU GGC UCC AGC AGU CGG AGG GCG CCU CAG ACA GGU AUC GUG GAU GAG UGC UGC UUC CGG AGC UGU GAU CUA AGG AGG CUG GAG AUG UAU UGC GCA CCC CUC AAG CCU GCC AAG UCA GCU CGC UCU GUC CGU GCC CAG CGC CAC ACC GAC AUG CCC AAG ACC CAG AAG GAA GUA CAU UUG AAG AAC GCA AGU AGA GGG AGU GCA GGA AAC AAG AAC UAC AGG AUG-3'.

5. A composition according to claim 3 wherein said nucleic acid molecules comprise the following sequence, wherein U can also be T:

5'-AUG GGA AUC CCA AUG GGG AAG UCG AUG CUG GUG CUU CUC ACC UUC UUG GCC UUC GCC UCG UGC UGC AUU GCU GCU UAC CGC CCC AGU GAG ACC CUG UGC GGC GGG GAG CUG GUG GAC ACC CUC CAG UUC GUC UGU GGG GAC CGC GGC UUC UAC UUC AGC AGG CCC GCA AGC CGU GUG AGC CGU CGC AGC CGU GGC AUC GUU GAG GAG UGC UGU UUC CGC AGC UGU GAC CUG GCC CUC CUG

26 FT 40" 600 ZC880

Sub  
B1

GAG ACG UAC UGU GCU ACC CCC GCC  
 AAG UCC GAG AGG GAC GUG UCG ACC  
 CCU CCG ACC GUG CUU CCG GAC AAC  
 UUC CCC AGA UAC CCC GUG GGC AAG  
 UUC UUC CAA UAU GAC ACC UGG AAG  
 CAG UCC ACC CAG CGC CUG CGC AGG  
 GGC CUG CCU GCC CUC CUG CGU GCC  
 CGC CGG GGU CAC GUG CUC GCC AAG  
 GAG CUC GAG GCG UUC AGG GAG GCC  
 AAA CGU CAC CGU CCC CUG AUU GCU  
 CUA CCC ACC CAA GAC CCC GGC CAC  
 GGG GGC GCC CCC CCA GAG AUG GCC  
 AGC AAU CGG AAG UGA-3'.

6. A composition according to claim 1 wherein said nucleic acid molecules are DNA.

7. A composition according to claim 1 wherein said nucleic acid molecules are RNA.

8. A composition comprising cellular hosts transformed by a heterologous DNA sequence substantially free of cellular hosts that do not contain said heterologous DNA sequence, wherein said heterologous DNA sequence is a human sequence encoding insulin-like growth factor (hIGF) selected from the group consisting of:

(a) 5'-GGA CCG GAG ACG CTC TGC GGG  
 GCT GAG CTG GTG GAT GCT CTT CAG  
 TTC GTG TGT GGA GAC AGG GGC TTT  
 TAT TTC AAC AAG CCC ACA GGG TAT  
 GGC TCC AGC AGT CGG AGG GCG CCT  
 CAG ACA GGT ATC GTG GAT GAG TGC  
 TGC TTC CGG AGC TGT GAT CTA AGG  
 AGG CTG GAG ATG TAT TGC GCA CCC  
 CTC AAG CCT GCC AAG TCA GCT-3';

(b) 5'-GCT TAC CGC CCC AGT GAG ACC CTG  
 TGC GGC GGG GAG CTG GTG GAC ACC  
 CTC CAG TTC GTC TGT GGG GAC CGC  
 GGC TTC TAC TTC AGC AGG CCC GCA  
 AGC CGT GTG AGC CGT CGC AGC CGT  
 GGC ATC GTT GAG GAG TGC TGT TTC  
 CGC AGC TGT GAC CTG GCC CTC CTG  
 GAG ACG TAC TGT GCT ACC CCC GCC  
 AAG TCC GAG-3';

(c) nucleic acid sequences complementary to (a) or (b); and

(d) fragments of (a), (b) or (c) that are at least 18 bases in length and which will selectively hybridize to human genomic DNA encoding hIGF.

9. A composition according to claim 8 wherein said heterologous DNA sequence is selected from the group consisting of (a), (b) and (c).

10. A composition according to claim 9 wherein said hIGF is hIGF-I and said heterologous DNA sequence is (a).

~~11. A composition according to claim 9 wherein said hIGF is hIGF-II and said heterologous DNA sequence is (b).~~

12. A composition according to claim 10 wherein said heterologous DNA sequence comprises the following sequence:

5'-CTG GCG CTG TGC CTG CTC ACC TTC  
 ACC AGC TCT GCC ACG GCT GGA CCG  
 GAG ACG CTC TGC GGG GCT GAG CTG  
 GTG GAT GCT CTT CAG TTC GTG TGT  
 GGA GAC AGG GGC TTT TAT TTC AAC  
 AAG CCC ACA GGG TAT GGC TCC AGC

Sub  
D3

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AGT CGG AGG GCG CCT CAG ACA GGT  
 ATC GTG GAT GAG TGC TGC TTC CGG  
 AGC TGT GAT CTA AGG AGG CTG GAG  
 ATG TAT TGC GCA CCC CTC AAG CCT  
 GCC AAG TCA GCT CGC TCT GTC CGT  
 GCC CAG CGC CAC ACC GAC ATG CCC  
 AAG ACC CAG AAG GAA GTA CAT TTG  
 AAG AAC GCA AGT AGA GGG AGT GCA  
 GGA AAC AAG AAC TAC AGG ATG-3'.

13. A composition according to claim 11 wherein said heterologous DNA sequence comprises the following sequence:

5'-ATG GGA ATC CCA ATG GGG AAG TCG  
 ATG CTG GTG CTT CTC ACC TTC TTG  
 GCC TTC GCC TCG TGC TGC ATT GCT  
 GCT TAC CGC CCC AGT GAG ACC CTG  
 TGC GGC GGG GAG CTG GTG GAC ACC  
 CTC CAG TTC GTC TGT GGG GAC CGC  
 GGC TTC TAC TTC AGC AGG CCC GCA  
 AGC CGT GTG AGC CGT CGC AGC CGT  
 GGC ATC GTT GAG GAG TGC TGT TTC  
 CGC AGC TGT GAC CTG GCC CTC CTG  
 GAG ACG TAC TGT GCT ACC CCC GCC  
 AAG TCC GAG AGG GAC GTG TCG ACC  
 CCT CCG ACC GTG CTT CCG GAC AAC  
 TTC CCC AGA TAC CCC GTG GGC AAG  
 TTC TTC CAA TAT GAC ACC TGG AAG  
 CAG TCC ACC CAG CGC CTG CGC AGG  
 GGC CTG CCT GCC CTC CTG CGT GCC  
 CGC CGG GGT CAC GTG CTC GCC AAG  
 GAG CTC GAG GCG TTC AGG GAG GCC  
 AAA CGT CAC CGT CCC CTG ATT GCT  
 CTA CCC ACC CAA GAC CCC GCC CAC  
 GGG GGC GCC CCC CCA GAG ATG GCC  
 AGC AAT CGG AAG TGA-3'.

14. A composition according to claim 9 wherein said heterologous DNA sequence is located on a plasmid that replicates in said cellular host.

15. A composition according to claim 9 wherein said cellular host is yeast.

16. A composition according to claim 9 wherein said cellular host is *E. coli*.

17. A composition according to claim 9 wherein said cellular host is *B. subtilis*.

18. A composition consisting essentially of nucleic acid molecules containing a human sequence encoding insulin-like growth factor (hIGF) selected from the group consisting of:

(a) 5'-GGA CCG GAG ACG CUC UGC GGG  
 GCU GAG CUG GUG GAU GCU CUU CAG  
 UUC GUG UGU GGA GAG AGG GGC UUU  
 UAU UUC AAC AAG CCC ACA GGG UAU  
 GGC UCC AGC AGU CGG AGG GCG CCU  
 CAG ACA GGU AUC GUG GAU GAG UGC  
 UGC UUC CGG AGC UGU GAU CUA AGG  
 AGG CUG GAG AUG UAU UGC GCA CCC  
 CUC AAG CCU GCC AAG UCA GCU-3',  
 wherein U can also be T;

(b) 5'-GCU UAC CGC CCC AGU GAG ACC CUG  
 UGC GGC GGG GAG CUG GUG GAC ACC  
 CUC CAG UUC GUC UGU GGG GAC CGC  
 GGC UUC UAC UUC AGC AGG CCC GCA

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Sub  
D3  
cmt

Sub  
B2

AGC CGU GUG AGC CGU CGC AGC CGU  
 GGC AUC GUU GAG GAG UGC UGU UUC  
 CGC AGC UGU GAC CUG GCC CUC CUG  
 GAG ACG UAC UGU GCU ACC CCC GCC  
 AAG UCC GAG-3', wherein U can also be T;

(c) nucleic acid sequences complementary to (a) or (b); and

(d) fragments of (a), (b) or (c) that are at least 18 bases in length and which will selectively hybridize to human genomic DNA encoding hIGF.

19. A composition according to claim 9 wherein said cellular host is *E. coli* HB101(phigf1).

20. A composition according to claim 1 wherein said nucleic acid molecules are phigf1.

21. A composition according to claim 9 wherein said cellular host is *E. coli* HB101(phigf2).

22. A composition according to claim 1 wherein said nucleic acid molecules are phigf2.

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